

## SEQUENCE LISTING



## (1) GENERAL INFORMATION:

## (i) APPLICANT:

- (A) NAME: THE SCRIPPS RESEARCH INSTITUTE
- (B) STREET: 10550 North Torrey Pines Road
- (C) CITY: La Jolla
- (D) STATE: California
- (E) COUNTRY: US
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(ii) TITLE OF INVENTION: MHC CLASS II ANTIGEN PRESENTING SYSTEMS  
AND METHODS FOR ACTIVATING CD4+ T CELLS

(iii) NUMBER OF SEQUENCES: 56

## (iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

## (v) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: PCT/US97/
- (B) FILING DATE: 22-MAY-1997
- (C) CLASSIFICATION:

## (vi) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 60/018,175
- (B) FILING DATE: 23-MAY-1996

## (2) INFORMATION FOR SEQ ID NO:1:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 740 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATTCGATGCA CACTCACATT CTTCTCCTAA TACGATAATA AAACCTTTCCA TGAAAAATAT	60
GGAAAAATAT ATGAAAATTG AGAAATCCAA AAAACTGATA AACGCTCTAC TTAATTAAAA	120
TAGATAAATG GGAGCGGCTG GAATGGCGGA GCATGACCAA GTTCCTCCGC CAATCAGTCG	180
TAAACAGAA GTCGTGGAAA GCGGATAGAA AGAATGTTTCG ATTTGACGGG CAAGCATGTC	240
TGCTATGTGG CGGATTGCGG AGGAATTGCA CTGGAGACCA GCAAGGTTCT CATGACCAAG	300
AATATAGCGG TGTGAGTGAG CGGGAAGCTC GGTTCGTGTC CAGATCGAAC TCAAACTAG	360
TCCAGCCAGT CGCTGTGCGA ACTAATTAAG TTAATGAGTT TTTCATGTTA GTTTCGCGCT	420
GAGCAACAAT TAAGTTTATG TTTTCAGTTCG GCTTAGATTT CGCTGAAGGA CTTGCCACTT	480
TCAATCAATA CTTTAGAACA AAATCAAAAC TCATTCTAAT AGCTTGGTGT TCATCTTTTT	540
TTTAAATGAT AAGCATTGTT TCGTTTATAC TTTTATATT TCGATATTAA ACCACCTATG	600
AAGTTCATTT TAATCGCCAG ATAAGCAATA TATTGTGTAA ATATTTGTAT TCTTTATCAG	660
GAAATTCAGG GAGACGGGGA AGTTACTATC TACTAAAAGC CAAACAATTT-CTTACAGTTT	720
TACTCTCTCT ACTCTAGAGT	740

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 427 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

AATTCGTTGC AGGACAGGAT GTGGTGCCCG ATGTGACTAG CTCTTTGCTG CAGGCCGTCC	60
TATCCTCTGG TTCCGATAAG AGACCCAGAA CTCCGGCCCC CCACCGCCCA CCGCCACCCC	120

CATACATATG TGGTACGCAA GTAAGAGTGC CTGCCGATGC CCCATGTGCC CCACCAAGAG	180
TTTTGCATCC CATACAAGTC CCCAAAGTGG AGAACCGAAC CAATTCTTCG CGGGCAGAAC	240
AAAAGCTTCT GCACACGTCT CCACTCGAAT TTGGAGCCGG CCGGCGTGTG CAAAAGAGGT	300
GAATCGAACG AAAGACCCGT GTGTAAAGCC GCGTTTCCAA AATGTATAAA ACCGAGAGCA	360
TCTGGCCAAT GTGCATCAGT TGTGGTCAGC AGCAAAATCA AGTGAATCAT CTCAGTGCAA	420
CTAAAGG	427

## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTTGAATTCC ACCATGCCGT GCAGCAGAGC TCTGA	35
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## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TTTGGATCCT CATAAAGGCC CTGGGTGTC	29
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## (2) INFORMATION FOR SEQ ID NO:5:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CTTGAATTCC ACCATGGCTC TGCAGATCCC CA

32

## (2) INFORMATION FOR SEQ ID NO:6:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TTTGGATCCT CACTGCAGGA GCCCTGCT

28

## (2) INFORMATION FOR SEQ ID NO:7:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4713 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GCGTTGCAGG ACAGGATGTG GTGCCCCGATG TGA TAGCTC TTTGCTGCAG GCCGTCCTAT	60
CCTCTGGTTC CGATAAGAGA CCCAGAACTC CGGCCCCCCA CCGCCCACCG CCACCCCCAT	120
ACATATGTGG TACGCAAGTA AGAGTGCCCTG CGCATGCCCC ATGTGCCCCA CCAAGAGTTT	180
TGCATCCCAT ACAAGTCCCC AAAGTGGAGA ACCGAACCAA TTCTTCGCGG GCAGAACAAA	240
AGCTTCTGCA CACGTCTCCA CTCGAATTTG GAGCCGGCCG GCGTGTGCAA AAGAGGTGAA	300
TGGAACGAAA GACCCGTGTG TAAAGCCGCG TTTCCAAAAT GTATAAAACC GAGAGCATCT	360
GGCCAATGTG CATCAGTTGT GGTGAGCAGC AAAATCAAGT GAATCATCTC AGTGCAACTA	420
AAGGGGGGAA TTCCTGCAGA GACCTCCCAG AGACCAGGAT GCCGTGCAGC AGAGCTCTGA	480
TTCTGGGGGT CCTCGCCCTG AACACCATGC TCAGCCTCTG CGGAGGTGAA GACGACATTG	540
AGGCCGACCA CGTAGGCTTC TATGGTACAA CTGTTTATCA GTCTCCTGGA GACATTGGCC	600
AGTACACACA TGAATTTGAT GGTGATGAGT TGTTCTATGT GGACTTGGAT AAGAAGAAAA	660
CTGTCTGGAG GCTTCCTGAG TTTGGCCAAAT TGATACTCTT TGAGCCCCAA GGTGGACTGC	720
AAAACATAGC TGCAGAAAAA CACAACCTGG GAATCTTGAC TAAGAGGTCA AATTTACCCC	780
CAGCTACCAA TGAGGCTCCT CAAGCGACTG TGTTCCCCAA GTCCCCTGTG CTGCTGGGTC	840
AGCCCAACAC CTTTATCTGC TTTGTGGACA ACATCTTCCC ACCTGTGATC AACATCACAT	900
GGCTCAGGAA TAGCAAGTCA GTCACAGACG GCGTTTATGA GACCAGCTTC CTCGTCAACC	960
GTGACCATT CTTCCACAAG CTGTCTTATC TCACCTTCAT CCCTTCTGAT GATGACATTT	1020
ATGACTGCAA GGTGGAGCAC TGGGGCCTGG AGGAGCCGGT TCTGAAACAC TGGGAACCTG	1080
AGATTCCAGC CCCCATGTCA GAGCTGACAG AAAGTGTGGT GTGTGCCCTG GGGTTGTCTG	1140
TGGGCCTTGT GGGCATCGTG GTGGGCACCA TCTTCATCAT TCAAGGCCTG CGATCAGGTG	1200
GCACCTCCAG ACACCCAGGG CCTTTATGAG TCACACCCTG GAAAGGAAGG TGTGTGTCCC	1260
TCTTCATGGA AGAAGTGGTG TTCTGGGTGT CGAATTCGAG CTCGGTACCC GGGGATCCTC	1320
TAGAGTCGAC CTGCAGGCAT GCAATTCGAT GCACACTCAC ATTCTTCTCC TAATACGATA	1380
ATAAACTTT CCATGAAAAA TATGGAAAAA TATATGAAAA TTGAGAAATC CAAAAAACTG	1440
ATAAACGCTC TACTTAATTA AAATAGATAA ATGGGAGCGG CAGGAATGGC GGAGCATGGC	1500
CAAGTTCCTC CGCCAATCAG TCGTAAACAA GAAGTCGTGG AAAGCGGATA GAAAGAATGT	1560
TCGATTTGAC GGGCAAGCAT GTCTGCTATG TGGCGGATTG CGGAGGAATT GCACTGGAGA	1620
CCAGCAAGGT TCTCATGACC AAGAATATAG CCGTGAGTGA GCGGGAAGCT CGGTTTCTGT	1680
CCAGATCGAA CTCAAAATA GTCCAGCCAG TCGCTGTGCA AACTAATTAA GTAAATGAGT	1740

TTTTCATGTT	AGTTTCGCGC	TGAGCAACAA	TTAAGTTTAT	GTTTCAGTTC	GGCTTAGATT	1800
TGCCTGAAGG	ACTTGCCACT	TTCAATCAAT	ACTTTAGAAC	AAAATCAAAA	CTCATTCTAA	1860
TAGCTTGGTG	TTTCATCTTT	TTTTTAATGA	TAAGCATTTT	GTCGTTTATA	CTTTTTATAT	1920
TTGATATTA	AACCACCTAT	GAAGTTCATT	TTAATCGCCA	GATAAGCAAT	ATATTGTGTA	1980
AATATTTGTA	TTCTTTATCA	GGAAATTCAG	GGAGACGGGG	AAGTTACTAT	CTACTAAAAG	2040
CCAAACAATT	TCTTACAGTT	TACTCTCTC	TACTCTAGAG	CTTGCCACTG	GGCGTCGTTT	2100
TACAACGTCG	TGACTGGGAA	AACCCTGGCG	TTACCCAAC	TAATCGCCTT	GCAGCACATC	2160
CCCCTTTCGC	CAGCTGGCGT	AATAGCGAAG	AGGCCCGCAC	CGATCGCCCT	TCCCAACAGT	2220
TGCGCAGCCT	GAATGGCGAA	TGGCGCCTGA	TGCGGTATTT	TCTCCTTACG	CATCTGTGCG	2280
GTATTTTACA	CCGCATATGG	TGCACTCTCA	GTACAATCTG	CTCTGATGCC	GCATAGTTAA	2340
GCCAGCCCCG	ACACCCGCCA	ACACCCGCTG	ACGCGCCCTG	ACGGGCTTGT	CTGCTCCCGG	2400
CATCCGCTTA	CAGACAAGCT	GTGACCGTCT	CGGGGAGCTG	CATGTGTCAG	AGGTTTTTCAC	2460
CGTCATCACC	GAAACGCGCG	AGACGAAAGG	GCCTCGTGAT	ACGCCTATTT	TTATAGGTTA	2520
ATGTCATGAT	AATAATGGTT	TCTTAGACGT	CAGGTGGCAC	TTTTCGGGGA	AATGTGCGCG	2580
GAACCCCTAT	TTGTTTATTT	TTCTAAATAC	ATTCAAATAT	GTATCCGCTC	ATGAGACAAT	2640
AACCCTGATA	AATGCTTCAA	TAATATTGAA	AAAGGAAGAG	TATGAGTATT	CAACATTTCC	2700
GTGTCGCCCT	TATTCCTTTT	TTTGCGGCAT	TTTGCCCTCC	TGTTTTTGCT	CACCCAGAAA	2760
CGCTGGTGAA	AGTAAAAGAT	GCTGAAGATC	AGTTGGGTGC	ACGAGTGGGT	TACATCGAAC	2820
TGGATCTCAA	CAGCGGTAAG	ATCCTTGAGA	GTTTTCGCCC	CGAAGAACGT	TTTCCAATGA	2880
TGAGCACTTT	TAAAGTTCTG	CTATGTGGCG	CGGTATTATC	CCGTATTGAC	GGCGGGCAAG	2940
AGCAACTCGG	TCGCCGCATA	CACTATTCTC	AGAATGACTT	GGTTGAGTAC	TCACCACTCA	3000
CAGAAAAGCA	TCTTACGGAT	GGCATGACAG	TAAGAGAATT	ATGCAGTGCT	GCCATAACCA	3060
TGAGTGATAA	CACTGCGGCC	AACTTACTTC	TGACAACGAT	CGGAGGACCG	AAGGAGCTAA	3120
CGGCTTTTTT	GCACAACATG	GGGGATCATG	TAAGTGGCCT	TGATCGTTGG	GAACCGGAGC	3180
TGAATGAAGC	CATACCAAAC	GACGAGCGTG	ACACCACGAT	GCCTGTAGCA	ATGGCAACAA	3240
CGTTGCGCAA	ACTATTAACT	GGCGAACTAC	TTACTCTAGC	TTCCCGGCAA	CAATTAATAG	3300
ACTGGATGGA	GGCGGATAAA	GTTGCAGGAC	CACTTCTGCG	CTCGGCCCTT	CCGGCTGGCT	3360
GGTTTATTGC	TGATAAATCT	GGAGCCGGTG	AGCGTGGGTC	TCGCGGTATC	ATTGCAGCAC	3420
TGGGGCCAGA	TGGTAAGCCC	TCCCGTATCG	TAGTTATCTA	CACGACGGGG	AGTCAGGCAA	3480
CTATGGATGA	ACGAAATAGA	CAGATCGCTG	AGATAGGTGC	CTCACTGATT	AAGCATTGGT	3540
AACTGTCAGA	CCAAGTTTAC	TCATATATAC	TTTAGATTGA	TTTAAACTTT	CATTTTTAAT	3600
TTAAAAGGAT	CTAGGTGAAG	ATCCTTTTTG	ATAATCTCAT	GACCAAATC	CCTTAACGTG	3660
AGTTTTTCGT	CCACTGAGCG	TCAGACCCCG	TAGAAAAGAT	CAAAGGATCT	TCTTGAGATC	3720
CTTTTTTTCT	GCGCGTAATC	TGCTGCTTGC	AAACAAAAAA	ACCACCGCTA	CCAGCGGTGG	3780
TTTGTTTGCC	GGATCAAGAG	CTACCAACTC	TTTTTCGGAA	GGTAACTGGC	TTGAGCAGAG	3840
CGCAGATACC	AAATACTGTC	CTTCTAGTGT	AGCCGTAGTT	AGGCCACCAC	TTCAAGAACT	3900
CTGTAGCACC	GCCTACATAC	CTCGCTCTGC	TAATCCTGTT	ACCAGTGGCT	GCTGCCAGTG	3960
GCGATAAGTC	GTGTCTTACC	GGGTGGGACT	CAAGACGATA	GTTACCGGAT	AAGGCGCAGC	4020
GGTCGGGCTG	AACGGGGGGT	TCGTGCACAC	AGCCCAGCTT	GGAGCGAACG	ACCTACACCG	4080

AACTGAGATA CCTACAGCGT GAGCATTGAG AAAGCGCCAC GCTTCCCGAA GGGAGAAAGG	4140
CGGACAGGTA TCCGTAAGC GGCAGGGTCG GAACAGGAGA GCGCAGGAGG GAGCTTCCAG	4200
GGGGAAACGC CTGGTATCTT TATAGTCCTG TCGGGTTTCG CCACCTCTGA CTTGAGCGTC	4260
GATTTTTGTG ATGCTCGTCA GGGGGGCGGA GCCTATGGAA AAACGCCAGC AACGCGGCCT	4320
TTTTACGGTT CCTGGCCTTT TGCTGGCCTT TTGCTCACAT GTTCTTTCCT GCGTTATCCC	4380
CTGATTCTGT GGATAACCGT ATTACCGCCT TTGAGTGAGC TGATACCGCT CGCCGCAGCC	4440
GAACGACCGA GCGCAGCGAG TCAGTGAGCG AGGAAGCGGA AGAGCGCCCA ATACGCAAAC	4500
CGCCTCTCCC CGCGCGTTGG CCGATTCATT AATGCAGCTG GCACGACAGG TTTCCCGACT	4560
GGAAAGCGGG CAGTGAGCGC AACGCAATTA ATGTGAGTTA GCTCACTCAT TAGGCACCCC	4620
AGGCTTTACA CTTTATGCTT CCGGCTCGTA TGTGTGTGG AATTGTGAGC GGATAACAAT	4680
TTACACAGG AAACAGCTAT GACCATGATT ACG	4713

## (2) INFORMATION FOR SEQ ID NO:8:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4724 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GCGTTGCAGG ACAGGATGTG GTGCCCCGATG TGA CTAGCTC TTTGCTGCAG GCCGTCTTAT	60
CCTCTGGTTC CGATAAGAGA CCCAGAACTC CGGCCCCCCA CCGCCCACCG CCACCCCCAT	120
ACATATGTGG TACGCAAGTA AGAGTGCCTG CGCATGCCCC ATGTGCCCCA CCAAGAGTTT	180
TGCATCCCAT ACAAGTCCCC AAAGTGGAGA ACCGAACCAA TTCTTCGGCG GCAGAACAAA	240
AGCTTCTGCA CAGTCTCCA CTCGAATTTG GAGCCGGCCG GCGTGTGCAA AAGAGGTGAA	300
TCGAACGAAA GACCCGTGTG TAAAGCCGCG TTTCCAAAAT GTATAAAACC GAGAGCATCT	360
GGCCAATGTG CATCAGTTGT GGTACGACAG AAAATCAAGT GAATCATCTC AGTGCAACTA	420
AAGGGGGGAA TTCCCTGCTG TGCCCTAGAG ATGGCTCTGC AGATCCCCAG CCTCCTCCTC	480
TCAGCTGCTG TGGTGGTGCT GATGGTGCTG AGCAGCCCAG GGA CTGAGGG CGGAAACTCC	540
GAAAGGCATT TCCTGGTCCA GTTCAAGGGC GAGTGCTACT ACACCAACGG GACGCAGCGC	600
ATACGGCTCG TGACCAGATA CATCTACAAC CGGGAGGAGT ACGTGCGCTA CGACAGCGAC	660
GTGGGCGAGT ACCGCGCGGT GACCGAGCTG GGGCGGCCAG ACGCCGAGTA CTGGAACAGC	720

CAGCCGGAGA	TCCTGGAGCG	AACGCCGGGCC	GAGGTGGACA	GGCGTGCAG	ACACAACACTAC	780
GAGGGGCGCG	AGACCAGCAC	CTCCCTGCCG	CGGCTTGAAC	AGCCCAATAT	CGCCATCTCC	840
CTGTCCAGGA	CAGAGGCCCT	CAACCACCAC	AACACTCTGG	TCTGTTCCGT	GACAGATTTT	900
TACCCAGCCA	AGATCAAAGT	GCGCTGGTTC	AGGAATGGCC	AGGAGGAGAC	AGTGGGGGTC	960
TCATCCACAC	AGCTTATTAG	GAATGGGGAC	TGGACCTTCC	AGGTCCTGGT	CATGCTGGAG	1020
ATGACCCCTC	ATCAGGGAGA	GGTCTACACC	TGCCATGTGG	AGCATCCCAG	CCTGAAGAGC	1080
CCCATCACTG	TGGAGTGGAG	GGCAGAGTCC	GAGTCTGCCC	GGAGCAAGAT	GTTGAGCGGC	1140
ATCGGGGGCT	GCGTGCTTGG	GGTGATCTTC	CTCGGGCTCG	GCCTTTTCAT	CCGTACACAGG	1200
AGTCAGAAAG	GACCTCGAGG	CCCTCCTCCA	GCAGGGCTCC	TGCAGTGAAT	CAGAGTGTTC	1260
TGACTCAGTT	GACTGTCTCA	GACTGTAAAG	CCTACATGTC	TGCAATTCTG	GCTCGGTACC	1320
CGGGGATCCT	CTAGAGTCGA	CCTGCAGGCA	TGCAATTCTG	TGCACACTCA	CATTCTTCTC	1380
CTAATACGAT	AATAAACTT	TCCATGAAAA	ATATGGAAAA	ATATATGAAA	ATTGAGAAAT	1440
CCAAAAAACT	GATAAACGCT	CTACTTAATT	AAAATAGATA	AATGGGAGCG	GCAGGAATGG	1500
CGGAGCATGG	CCAAGTTCCT	CCGCCAATCA	GTCGTAAAC	AGAAGTCGTG	GAAAGCGGAT	1560
AGAAAGAATG	TTGATTTGA	CGGGCAAGCA	TGTCTGCTAT	GTGGCGGATT	GCGGAGGAAT	1620
TGCACTGGAG	ACCAGCAAGG	TTCTCATGAC	CAAGAATATA	GCGGTGAGTG	AGCGGGAAGC	1680
TGGTCTTCTG	TCCAGATCGA	ACTCAAACT	AGTCCAGCCA	GTCGCTGTCT	AACTAATTA	1740
AGTAAATGAG	TTTTTCATGT	TAGTTTCGCG	CTGAGCAACA	ATTAAGTTTA	TGTTTCAGTT	1800
CGGCTTAGAT	TTGCTGAAG	GACTTGCCAC	TTTCAATCAA	TACTTTAGAA	CAAAATCAAA	1860
ACTCATTCTA	ATAGCTTGGT	GTTTCATCTT	TTTTTTAATG	ATAAGCATTT	TGTCGTTTAT	1920
ACTTTTTATA	TTTCGATATT	AAACCACCTA	TGAAGTTCAT	TTTAATCGCC	AGATAAGCAA	1980
TATATTGTGT	AAATATTTGT	ATTCTTTATC	AGGAAATTCA	GGGAGACGGG	GAAGTTACTA	2040
TCTACTAAAA	GCCAAACAAT	TTCTTACAGT	TTTACTCTCT	CTACTCTAGA	GCTTGGCACT	2100
GGCGTCGTT	TTACAACGTC	GTGACTGGGA	AAACCCTGGC	GTTACCCAAC	TTAATCGCCT	2160
TGCAGCACAT	CCCCCTTTCG	CCAGCTGGCG	TAATAGCGAA	GAGGCCCCGA	CCGATCGCCC	2220
TTCCCAACAG	TTGCGCAGCC	TGAATGGCGA	ATGGCGCCTG	ATGCGGTATT	TTCTCCTTAC	2280
GCATCTGTGC	GGTATTTTAC	ACCGCATATG	GTGCACTCTC	AGTACAATCT	GCTCTGATGC	2340
CGCATAGTTA	AGCGAGCCCC	GACACCCGCC	AACACCCGCT	GACGCGCCCT	GACGGGCTTG	2400
TCTGCTCCCG	GCATCCGCTT	ACAGACAAGC	TGTGACCGTC	TCCGGGAGCT	GCATGTGTCA	2460
GAGGTTTTCA	CCGTCATCAC	CGAAACGCGC	GAGACGAAAG	GGCCTCGTGA	TACGCCTATT	2520
TTTATAGGTT	AATGTCATGA	TAATAATGGT	TTCTTAGACG	TCAGGTGGCA	CTTTTCGGGG	2580
AAATGTGCGC	GGAACCCCTA	TTTGTTTATT	TTTCTAAATA	CATTCAAATA	TGTATCCGCT	2640
CATGAGACAA	TAACCTGAT	AAATGCTTCA	ATAATATTGA	AAAAGGAAGA	GTATGAGTAT	2700
TCAACATTTT	CGTGTCGCCC	TTATTCCCTT	TTTTGCGGCA	TTTTGCCTTC	CTGTTTTTGC	2760
TCACCCAGAA	ACGCTGGTGA	AAGTAAAAGA	TGCTGAAGAT	CAGTTGGGTG	CACGAGTGGG	2820
TTACATCGAA	CTGGATCTCA	ACAGCGGTAA	GATCCTTGAG	AGTTTTCGCC	CCGAAGAACG	2880
TTTTCCAATG	ATGAGCACTT	TTAAAGTTCT	GCTATGTGGC	GCGGTATTAT	CCCGTATTGA	2940
CGCCGGGCAA	GAGCAACTCG	GTGCGCGCAT	ACACTATTCT	CAGAATGACT	TGGTTGAGTA	3000
CTCACCAGTC	ACAGAAAAGC	ATCTTACGGA	TGGCATGACA	GTAAGAGAAT	TATGCAGTGC	3060



TGCCATAACC ATGAGTGATA ACACTGCGGC CAACTTACTT CTGACAACGA TCGGAGGACC	3120
GAAGGAGCTA ACCGCTTTTT TGCACAACAT GGGGGATCAT GTAAC TCGCC TTGATCGTTG	3180
GGAACCGGAG CTGAATGAAG CCATACCAAA CGACGAGCGT GACACCACGA TGCCTGTAGC	3240
AATGGCAACA ACGTTGCGCA AACTATTAAC TGGCGAACTA CTTACTCTAG CTTCCCGGCA	3300
ACAATTAATA GACTGGATGG AGGCGGATAA AGTTGCAGGA CCACTTCTGC GCTCGGCCCT	3360
TCCGGCTGGC TGGTTTATTG CTGATAAATC TGGAGCCGGT GAGCGTGGGT CTGCGGGTAT	3420
CATTGCAGCA CTGGGGCCAG ATGGTAAGCC CTCCCGTATC GTAGTTATCT ACACGACGGG	3480
GAGTCAGGCA ACTATGGATG AACGAAATAG ACAGATCGCT GAGATAGGTG CCTCACTGAT	3540
TAAGCATTGG TAACTGTCAG ACCAAGTTTA CTCATATATA CTTTAGATTG ATTTAAAACT	3600
TCATTTTTAA TTTAAAAGGA TCTAGGTGAA GATCCTTTTT GATAATCTCA TGACCAAAAT	3660
CCCTTAACGT GAGTTTTTCGT TCCACTGAGC GTCAGACCCC GTAGAAAAGA TCAAAGGATC	3720
TTCTTGAGAT CCTTTTTTTC TGGCGGTAAT CTGCTGCTTG CAAACAAAAA AACCACCGCT	3780
ACCAGCGGTG GTTTGTTTGC CGGATCAAGA GCTACCAACT CTTTTCCGA AGGTAAGTGG	3840
CTTCAGCAGA GCGCAGATAC CAAATACTGT CCTTCTAGTG TAGCCGTAGT TAGGCCACCA	3900
CTTCAAGAAC TCTGTAGCAC CGCCTACATA CCTCGCTCTG CTAATCCTGT TACCAGTGGC	3960
TGCTGCCAGT GCGGATAAGT CGTGTCTTAC CGGGTTGGAC TCAAGACGAT AGTTACCGGA	4020
TAAGGCGCAG CGGTCGGGCT GAACGGGGGG TTCGTGCACA CAGCCCAGCT TGGAGCGAAC	4080
GACCTACACC GAACTGAGAT ACCTACAGCG TGAGCATTGA GAAAGCGCCA CGCTTCCCGA	4140
AGGGAGAAAG GCGGACAGGT ATCCGGTAAG CGGCAGGGTC GGAACAGGAG AGCGCACGAG	4200
GGAGCTTCCA GGGGAAACG CCTGGTATCT TTATAGTCCT GTCGGGTTTC GCCACTCTG	4260
ACTTGAGCGT CGATTTTGTG GATGCTCGTC AGGGGGGCGG AGCCTATGGA AAAACGCCAG	4320
CAACGCGGCC TTTTACGGT TCCTGGCCTT TTGCTGGCCT TTTGCTCACA TGTTCTTTCC	4380
TGCGTTATCC CCTGATTCTG TGGATAACCG TATTACCGCC TTTGAGTGAG CTGATACCGC	4440
TCGCCGCAGC CGAACGACCG AGCGCAGCGA GTCAGTGAGC GAGGAAGCGG AAGAGCGCCC	4500
AATACGCAAA CCGCTCTCC CCGCGCGTTG GCCGATTGAT TAATGCAGCT GGCACGACAG	4560
GTTTCCCGAC TGGAAGCGG GCAGTGAGCG CAACGCAATT AATGTGAGTT AGCTCACTCA	4620
TTAGGCACCC CAGGCTTTAC ACTTTATGCT TCCGGCTCGT ATGTTGTGTG GAATTGTGAG	4680
CGGATAACAA TTTACACAG GAAACAGCTA TGACCATGAT TACG	4724

## (2) INFORMATION FOR SEQ ID NO:9:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CCACCATGGC CATTAGTGGA GTC

23

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TTTGATCCT TACAGAGGCC CCCTGCGTT

29

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CCACCATGGT GTGTCTGAGG CTCC

24

## (2) INFORMATION FOR SEQ ID NO:12:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TTTGATCCT CAGCTCAGGA ATCCTCTTG

29

## (2) INFORMATION FOR SEQ ID NO:13:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GCACCATGGT CCTAAACAAA GCTCTGAT

28

## (2) INFORMATION FOR SEQ ID NO:14:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TTGGATCCT CACAAGGGCC CTGGTGTCT

30

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CCACCATGGC TTGAAGAAG GCCTTT

26

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TTTAGATCTC AGTGCAGAAG CCCTTT

26

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CCACCATGGG CCCTGAAGAC AGAAT

25

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TTTGGATCCT CACAGGGTCC CCTGGGC

27

## (2) INFORMATION FOR SEQ ID NO:19:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CCACCATGGT TCTGCAGGTT TCTGCC

26

## (2) INFORMATION FOR SEQ ID NO:20:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TTTGGATCCT TATGCAGATC CTCGTTGAA

29

## (2) INFORMATION FOR SEQ ID NO:21:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

AAGAATTCAC TAGAGGCTAG AGCCAT

26

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

AAGGATCCTC ACAGGGTGAC TTGACC

26

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2580 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GCGTTGCAGG ACAGGATGTG GTGCCCGATG TGA CTAGCTC TTTGCTGCAG GCCGTCCTAT	60
CCTCTGGTTC CGATAAGAGA CCCAGAACTC GGGCCCCCA CCGCCCACCG CCACCCCAT	120
ACATATGTGG TACGCAAGTA AGAGTGCCCTG CGCATGCCCC ATGTGCCCCA CCAAGAGTTT	180
TGCATCCCAT ACAAGTCCCC AAAGTGGAGA ACCGAACCAA TTCTTCGCGG GCAGAACAAA	240
AGTTCTGCA CACGTCTCCA CTCGAATTTG GAGCCGGCCG GCGTGTGCAA AAGAGGTGAA	300
TCGAACGAAA GACCCGTGTG TAAAGCCGGC TTTCCAAAAT GTATAAAACC GAGAGCATCT	360
GGCCAATGTG CATCAGTTGT GGTGAGCAGC AAAATCAAGT GAATCATCTC AGTGCAACTA	420
AAGGGGGGAA TTCGATCTAG AGGCTAGAGC CATGGATGAC CAACGCGACC TCATCTCTAA	480
CCATGAGCAA TTGCCATAC TGGGCAACCG CCCTAGAGAG CCAGAAAGGT GCAGCCGTGG	540
AGCTCTGTAC ACCGGTGTTT CTGTCTGGT GGCTCTGCTC TTGGCTGGGC AGGCCACCAC	600
TGCTTACTTC CTGTACCAGC AACAGGGCCG CCTAGACAAG CTGACCATCA CCTCCAGAA	660
CCTGCAACTG GAGAGCCTTC GCATGAAGCT TCCGAAATCT GCCAACCTG TGAGCCAGAT	720
GCGGATGGCT ACTCCCTTGC TGATGCGTCC AATGTCCATG GATAACATGC TCCTTGGGCC	780
TGTGAAGAAC GTTACCAAGT ACGGCAACAT GACCCAGGAC CATGTGATGC ATCTGCTCAC	840
GAGGTCTGGA CCCCTGGAGT ACCCGCAGCT GAAGGGGACC TTCCCAGAGA ATCTGAAGCA	900
TCTTAAGAAC TCCATGGATG GCGTGAAGT GAAGATCTTC GAGAGCTGGA TGAAGCAGTG	960
GCTCTTGTTT GAGATGAGCA AGAACTCCCT GGAGGAGAAG AAGCCACAG AGGCTCCACC	1020
TAAAGAGCCA CTGGACATGG AAGACCTATC TTCTGGCCTG GGAGTGACCA GGCAGGAACT	1080
GGGTCAAGTC ACCCTGTGAA GACAGAGGCC AGCATCAAGC TTATCGATAC CGTCGACCTG	1140
CAGGCATGCA ATTGATGCA CACTCACATT CTCTCTCTAA TACGATAATA AAACCTTCCA	1200
TGAAAAATAT GGAAAAATAT ATGAAAATTG AGAAATCCAA AAAACTGATA AACGCTCTAC	1260
TTAATTAAAA TAGATAAATG GGAGCGGCAG GAATGGCGGA GCATGGCCAA GTTCTCCGC	1320
CAATCAGTCG TAAAACAGAA GTCGTGGAAG GCGGATAGAA AGAATGTTTG ATTTGACGGG	1380
CAAGCATGTC TGCTATGTGG CGGATTGCGG AGGAATTGCA CTGGAGACCA GCAAGGTTCT	1440
CATGACCAAG AATATAGCGG TGAGTGAGCG GGAAGCTCGG TTTCTGTCCA GATCGAACTC	1500
AAAAC TAGTC CAGCCAGTCG CTGTCGAAAC TAATTAAAGTA AATGAGTTTT TCATGTTAGT	1560
TTGCGCTGA GCAACAATTA AGTTTATGTT TCAGTTCCGC TTAGATTTG CTGAAGGACT	1620
TGCCACTTTC AATCAATACT TTAGAACAAA ATCAAACTC ATTCTAATAG CTTGGTGTTT	1680
ATCTTTTTTT TTAATGATAA GCATTTTGTC GTTTATACCT TTTATATTTG GATATTAAAC	1740
CACCTATGAA GTTCATTTTA ATCGCCAGAT AAGCAATATA TTGTGTAAAT ATTTGTATT	1800
TTTATCAGGA AATTCAGGGA GACGGGGAAG TTA CTATCTA CTAAGGCCA AACAATTTCT	1860
TACAGTTTTA CTCTCTCTAC TCTAGAGCTT GGCAGTGGC GTCGTTTTAC AACGTCGTGA	1920
CTGGGAAAC CCTGGCGTTA CCCAACTTAA TCGCCTTGCA GCACATCCCC CTTTCGCCAG	1980
CTGGCGTAAT AGCGAAGAGG CCCGCACCGA TCGCCCTTCC CAACAGTTGC GCAGCCTGAA	2040
TGGCGAATGG CGCCTGATGC GGTATTTTCT CCTTACGCAT CTGTGCGGTA TTTCACACCG	2100



CATATGGTGC ACTCTCAGTA CAATCTGCTC TGATGCCGCA TAGTTAAGCC AGCCCCGACA	2160
CCCCCAACA CCCGCTGACG CGCCCTGACG GGCTTGTCTG CTCCGGGCAT CCGCTTACAG	2220
ACAAGCTGTG ACCGTCTCCG GGAGCTGCAT GTGTCAGAGG TTTTCACCGT CATCACCAGAA	2280
ACGCGCGAGA CGAAAGGGCC TCGTGATACG CCTATTTTTA TAGGTTAATG TCATGATAAT	2340
AATGGTTTCT TAGACGTCAG GTGGCACTTT TCGGGGAAAT GTGCGCGGAA CCCCTATTTG	2400
TTTATTTTTC TAAATACATT CAAATATGTA TCCGCTCATG AGACAATAAC CCTGATAAAT	2460
GCTTCAATAA TATTGAAAAA GGAAGAGTAT GAGTATTCAA CATTTCCGTG TCGCCCTTAT	2520
TCCCTTTTTT GCGGCATTTT GCCTTCCTGT TTTGCTCAC CCAGAAACGC TGGTGAAAGT	2580

## (2) INFORMATION FOR SEQ ID NO:24:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

AAGAATTCAC CATGGATGAT CAGCGCGACC TT

32

## (2) INFORMATION FOR SEQ ID NO:25:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

AAAGGATCCT CACATGGGGA CTGGGCCCAG A

31

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

AAACCATGGG TCATGAACAG AACCA

25

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TTTGTCGACT CAGTCACCTG AGCAAGG

27

(2) INFORMATION FOR SEQ ID NO:28:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AAACCATGGT CTCATTCCTG CC

22

## (2) INFORMATION FOR SEQ ID NO:29:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

TTTGTCGACC TAGGAAATGT GCCATCC

27

## (2) INFORMATION FOR SEQ ID NO:30:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TTTAGAATTC ACCATGGCTT CAACCCGTGC CAAG

34

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TTTAGTCGAC TCAGGGAGGT GGGGCTTGTC C

31

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

ACCCTTGAAT TCATGGCTCC CAGCAGCCCC CGGCCC

36

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

ATTACCGGAT CCTCAGGGAG GCGTGGCTTG TGTGTTCCG

39

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

AAGGTACCCG TGGAGACTGC CAGAGAT

27

(2) INFORMATION FOR SEQ ID NO:35:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

TTTGGATCCC TATGCCCGGA AGGCCTG

27

## (2) INFORMATION FOR SEQ ID NO:36:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

AAGAATTCCT GTCAGAATGG CCACCAT

27

## (2) INFORMATION FOR SEQ ID NO:37:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

TTTAGATCTT CACTCAGCTC TGGACGGT

28

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

ACCCTTGAGC TCATGGTTGC TGGGAGCGAC GCGGGG

36

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 42 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

ATTACCGGAT CCTTAAAGAA CATTATATA CAGCACAATA CA

42

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

TTTAGAATTC ACCATGGCTT GCAATTGTCA GTTG

34

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

TTTAGTCGAC CTAAAGGAAG ACGGTCTGTT C

31

(2) INFORMATION FOR SEQ ID NO:42:



## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

ACCCTTGAAT CCATGGGCCA CACACGGAGG CAG

33

## (2) INFORMATION FOR SEQ ID NO:43:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

ATTACCGGAT CCTTATACAG GCGTACACT TTCCCTTCT

39

## (2) INFORMATION FOR SEQ ID NO:44:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

TTTAGAATTC ACCATGGACC CCAGATGCAC CATGGG

36

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

TTTAGTCGAC TCACTCTGCA TTTGGTTTTG CTGA

34

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

ACCCTTGAGC TCATGGATCC CCAGTGCACT ATG

33

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 42 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

ATTACCCCGG GGTAAAAAC ATGTATCACT TTTGTGCAT GA

42

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

AAAGGATCCA CCATGCAGCA GCCCTTCAAT T

31

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

TTTGGATCCT TAGAGCTTAT ATAAGCCGA

29

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

AAAGAATTTCG GTACCATGCC GGAGGAGGGT TCGG

34

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

TTTGGATCCT CAGGGGCGCA CCCACTGCA

29

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Ile	Ser	Gln	Ala	Val	His	Ala	Ala	His	Ala	Glu	Ile	Asn	Glu	Ala	Gly
1				5					10					15	

Arg

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Pro Lys Tyr Val Lys Gln Asn Thr Leu Lys Leu Ala Thr  
1 5 10

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Lys Thr Ile Ala Thr Asp Glu Glu Ala Arg Arg  
1 5 10

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Gln Ala Ser Leu Ala Leu Ser Tyr Arg Leu Asn Met Phe Thr Pro  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Phe	Val	Arg	Phe	Asp	Ser	Asp	Ala	Ala	Ser	Gln	Arg	Met
1				5						10		